SEARCH NOTES

14 JUN 02

09/899,082

Databases searched: USPATFULL via EAST, Caplus, Medline, Biosis

Reviewed Parent Application(s) : 09/378,900 and 09/044,665

Search terms:

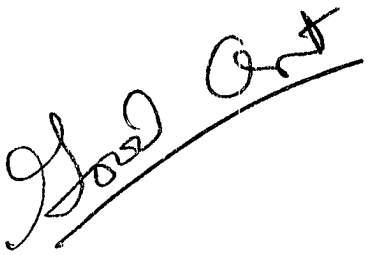
Inventor(s) : e.g. Maertens G?/au

STIC searched SEQ ID NOs : 1-4, 20 and 27

HCV

Hybridization

Amplification or PCR



SEQ ID NO: 1

```
RESULT   5
I73300
LOCUS       I73300                    51 bp    DNA     linear   PAT
03-APR-1998
DEFINITION  Sequence 31 from patent US 5686272.
ACCESSION   I73300
VERSION     I73300.1  GI:3009439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
  TITLE     Amplification of RNA sequences using the ligase chain reaction
  JOURNAL   Patent: US 5686272-A 31 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="unknown"
BASE COUNT       14 a     16 c     10 g     11 t
ORIGIN


  Query Match             98.5%;  Score 26.6;  DB 6;  Length 51;
  Best Local Similarity   96.3%;  Pred. No. 0.036;
  Matches   26;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 CCCTGTGAGGAACTWCTGTCTTCACGC 27
           |||||||||||||:|||||||||||||
Db      16 CCCTGTGAGGAACTACTGTCTTCACGC 42
```

SEQ ID NO: 1

RESULT 15
AAA75294
ID AAA75294 standard; cDNA; 308 BP
AC AAA75294;
DT 15-JAN-2001 (first entry)
DE Novel hepatitis C virus cDNA clone 18g.
KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
KW viral infectivity; viral replication; ds.
XX
OS Hepatitis C virus.
XX
PN EP1034785-A2.
XX
PD 13-SEP-2000.
XX
PF 16-MAR-1990; 2000EP-0109602.
XX
PR 17-MAR-1989; 89US-0325338.
PR 20-APR-1989; 89US-0341334.
PR 18-MAY-1989; 89US-0355002.
PR 16-MAR-1990; 90EP-0302866.
XX
PA (CHIR) CHIRON CORP.
XX
PI Houghton M, Choo Q, Kuo G;
XX
DR WPI; 2000-566891/53.
XX
PT Novel composition comprising a hepatitis C virus antisense
PT polynucleotide which is complementary to or corresponds to a sense
PT strand of the virus genome, and selectively hybridises to it -
XX
PS Example; Fig 14; 75pp; English.
XX
CC The specification describes a pharmaceutical composition which
CC comprises a hepatitis C virus (HCV) antisense polynucleotide. The
CC HCV is characterized by a positive stranded RNA genome which has
CC 40% homology at the polypeptide level to a HCV polyprotein. The
CC antisense polynucleotide binds to cellular polynucleotides which
CC enhance and/or are required for viral infectivity, replicative
CC ability or chronicity. The antisense polynucleotides may also be
CC designed to bind with high specificity, to be of increased stability,
CC to be stable and to have low toxicity. The composition also comprises
CC an agent which causes viral RNA to be inactive. The composition
CC is used for preventing HCV replication in a system. The present
CC sequence represents a novel HCV cDNA sequence, which is used in the
CC course of the invention.
XX
SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 other;

Query Match 98.5%; Score 26.6; DB 21; Length 308;
Best Local Similarity 96.3%; Pred. No. 0.011;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCCTGTGAGGAACTWCTGTCTTCACGC 27
           |||||||||||||:|||||||||||||
Db      19 ccctgtgaggaactactgtcttcacgc 45
```

SEQ ID NO: 1

```
RESULT   9
HPCBR56A
LOCUS       HPCBR56A                  296 bp    RNA     linear   VRL
03-FEB-1999
DEFINITION  Hepatitis C virus RNA, 5'untranslated region.
ACCESSION   D13448
VERSION     D13448.1  GI:435625
KEYWORDS    5' untranslated region.
SOURCE      Hepatitis C virus (isolate:BR56) cDNA to genomic RNA.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage;
Flaviviridae;
            Hepacivirus.

REFERENCE   2  (sites)
  AUTHORS   Bukh,J., Purcell,R.H. and Miller,R.H.
  TITLE     Sequence analysis of the 5' noncoding region of hepatitis C virus
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
  MEDLINE   92279243
FEATURES             Location/Qualifiers
     source          1. .296
                     /organism="Hepatitis C virus"
                     /isolate="BR56"
                     /db_xref="taxon:11103"
BASE COUNT       53 a     88 c     94 g     61 t
ORIGIN


  Query Match             98.5%;  Score 26.6;  DB 14;  Length 296;
  Best Local Similarity   96.3%;  Pred. No. 0.027;
  Matches   26;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 CCCTGTGAGGAACTWCTGTCTTCACGC 27
           ||||||||||||||:||||||||||||
Db       6 CCCTGTGAGGAACTTCTGTCTTCACGC 32
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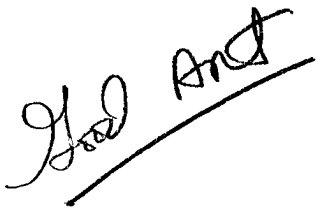

SEQ ID NO: 2

```
RESULT   2
AAQ85918
ID   AAQ85918 standard; DNA; 21 BP.
XX
AC   AAQ85918;
XX
DT   02-NOV-1995  (first entry)
XX
DE   Hepatitis C virus genome external PCR primer YK-104.
XX
KW   Hepatitis C virus; HCV; non-A non-B; external PCR primer;
KW   YK-104; primer specific detection; ss.
XX
OS   Synthetic.
XX
PN   WO9506753-A.
XX
PD   09-MAR-1995.
XX
PF   02-SEP-1994;   94WO-US09869.
XX
PR   03-SEP-1993;   93US-0116344.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-115465/15.
XX
PT   New method and kit for primer-specific detection of nucleic acids
PT    - using two primers having a known sequence and a marker, resp
PT   for solid-phase detection of amplification prods.
XX
PS   Example 1; Page 11; 20pp; English.
XX
CC   AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for
CC   the Hepatitis C virus (HCV) genome. They were used to demonstrate
CC   a new method for the primer specific detection of nucleic acids.
XX
SQ   Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGTGCACGGTCTACGAGACCT 21
           |||||||||||||||||||||
Db       1 ggtgcacggtctacgagacct 21
```

SEQ ID NO: 2

RESULT 6
AAQ67081
ID AAQ67081 standard; DNA; 25 BP.
XX
AC AAQ67081;
XX
DT 14-MAR-1995 (first entry)
XX
DE Antisense primer for amplifying Hepatitis C virus DNA fragment.
XX
KW Hepatitis C virus; restriction endonuclease; KpnI; marker;
KW cleavage site; HCV; ss.
XX
OS Synthetic.
XX
PN JP06181764-A.
XX
PD 05-JUL-1994.
XX
PF 20-JAN-1993; 93JP-0007721.
XX
PR 22-SEP-1992; 92JP-0252793.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
DR WPI; 1994-251687/31.
XX
PT DNA contg. KPNI recognition site as marker for hepatitis C virus
PT - useful in diagnosis of HC
XX
PS Disclosure; Page 8; 9pp; Japanese.
XX
CC Two primers (AAQ67080, AAQ67081) were used to amplify the sequence
CC described in AAQ67079 which is obtained from hepatitis C virus (HCV)
CC and comprises a KpnI restriction endonuclease recognition site.
CC The restriction site is found in the wild type sequence and can
CC therefore be used as a diagnostic marker.
XX
SQ Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACGGTCTACGAGACCT 21
||||||||||||||||||||
Db 3 ggtgcacggtctacgagacct 23

SEQ ID NO: 2

```
RESULT   5
US-08-441-971-33/c
; Sequence 33, Application US/08441971
; Patent No. 6071693
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS Version 3.3
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,971
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,653
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/881,528
;      FILING DATE:
;      APPLICATION NUMBER:  07/697,326
;      FILING DATE:  8 May 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Janiuk, Anthony J.
;      REGISTRATION NUMBER:  29,809
;      REFERENCE/DOCKET NUMBER:  C0772/7000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;      TELEX:  EZEKIEL
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    ORIGINAL SOURCE:  (ATCC # 40394)
;      INDIVIDUAL ISOLATE:  hcv1
US-08-441-971-33
  Query Match             100.0%;  Score 21;  DB 3;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGTGCACGGTCTACGAGACCT 21
           |||||||||||||||||||||
Db     252 GGTGCACGGTCTACGAGACCT 232
```

SEQ ID NO: 2

```
RESULT   9
AAQ43112
ID   AAQ43112 standard; DNA; 29 BP.
XX
AC   AAQ43112;
XX
DT   23-SEP-1993  (first entry)
XX
DE   HCV 5'NCR antisense primer 209.
XX
KW   Non-coding region; hepatitis C virus; blood donor; type 2; type 1;
KW   HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3;
KW   PCR; amplify; polymerase chain reaction; primer; NS4; ss.
XX
OS   Synthetic.
XX
PN   WO9310239-A.
XX
PD   27-MAY-1993.
XX
PF   20-NOV-1992;   92WO-GB02143.
XX
PR   21-NOV-1991;   91GB-0024696.
PR   24-JUN-1992;   92GB-0013362.
XX
PA   (COMM-) COMMON SERVICES AGENCY.
XX
PI   Chan S,  Simmonds P,  Yap PL;
XX
DR   WPI; 1993-182554/22.
XX
PT   DNA encoding antigenic peptide(s) of new types of hepatitis C
PT   virus - for diagnosing and treating HCV infection, screening
PT   blood samples and identifying different HCV types
XX
PS   Disclosure; Page 27; 120pp; English.
XX
CC   The sequences given in AAQ43112-33 are primers which were used to
CC   amplify specific regions of the hepatitis C virus (HCV) genome.
CC   Analysis of regions of the HCV genome revealed the existance of
CC   three distinct groups of HCV.  Analysis of the region encompassing
CC   -255 to -62 of the 5' non coding region (NCR) (see AAQ43058-75) showed
CC   a difference of 9-14% in the nucleotide sequences between the three
CC   groups.  Two of the groups identified were similar to those of HCV
CC   varients termed type 1 and 2, whilst the third appeared to represent
CC   a novel type of virus.  Comparison of the NS3 region (see AAR37927-30)
CC   showed a high degree of sequence diversity with type 3 being phylo-
CC   genetically different to type 1 and 2.  The same degree different-
CC   iation was noted in the NS-5 (see AAR37923-26), core region (see
CC   AAR37931) and the NS4 region (see AAQ43106-111) between type 3 and type
CC   1 sequences.
XX
SQ   Sequence 29 BP; 7 A; 8 C; 8 G; 6 T; 0 other;
  Query Match             100.0%;  Score 21;  DB 14;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
 Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
Qy       1 GGTGCACGGTCTACGAGACCT 21
           |||||||||||||||||||||
Db       9 ggtgcacggtctacgagacct 29
```